



(1) GENERAL INFORMATION:

- (i) APPLICANT: Simons, Michael
Volk, Rudiger
Horowitz, Arie
- (ii) TITLE OF INVENTION: Stimulation of angiogenesis
via enhanced endothelial expression of syndecan-4
core proteins
- (iii) NUMBER OF SEQUENCES: 24
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: David Prashker, Esq.
(B) STREET: P.O. Box 5387
(C) CITY: Magnolia
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 01930
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
(B) COMPUTER: Dell PC
(C) OPERATING SYSTEM: MS DOS
(D) SOFTWARE: Microsoft Word version 97
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/145,916
(B) FILING DATE: September 2, 1998
(C) CLASSIFICATION: Unknown
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: David Prashker, Esq.
(B) REGISTRATION NUMBER: 29,693
(C) REFERENCE/DOCKET NUMBER: BIS-039
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (978) 525-3794

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGACGTG CGGCGCTCTG GCTTTGGCTC TGC GCGCTGG CGCTGCGCCT GCAGCCTGCC 60
CTCCCGCAA TTGTCACCGC AAATGTGCCT CCTGAAGACC AAGATGGCTC TGGGGACGAC 120
TCAGACA ACT TCTCTGGCTC AGGCACAGGT GCTTTGCCAG ATATGACTTT GTCACGGCAG 180
ACACCTTCCA CTTGGAAGGA TGTGTGGCTC CTGACAGCTA CACCCACAGC TCCAGAACCC 240
ACCAGCAGGG ATACCGAGGC CACCCTCACC TCTATCCTGC CGGCTGGAGA GAAGCCTGAG 300
GAGGGAGAGC CCGTGGCCCA CGTGGAAGCA GAGCCTGACT TCACTGCTCG GGACAAGGAG 360
AAGGAGGCCA CCACCAGGCC TAGGGAGACC ACACAGCTCC CAGTCACCCA ACAGGCCTCA 420
ACAGCAGCCA GAGCCACCAC GGCCAGGCA TCTGTCACGT CTCATCCCCA CGGGGATGTG 480
CAACCTGGCC TCCACGAGAC CTTGGCTCCC ACAGCACCCG GCCAACCTGA CCATCAGCCT 540
CCAAGTGTGG AGGATGGAGG CACTTCTGTC ATCAAAGAGG TTGTGGAGGA TGAAACTACC 600
AATCAGCTTC CTGCAGGAGA GGGCTCTGGA GAACAAGACT TCACCTTTGA AACATCTGGG 660
GAGAACACAG CTGTGGCTGG CGTCGAGCCT GACCTTCGGA ATCAGTCCCC AGTGGATGAA 720
GGAGCCACAG GTGCTTCTCA GGCCTTTTG GACAGGAAGG AA 762

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1020 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCAGGAGGG AGGGAGCCAG AGGAAAAGAA GAGGAGGAGA AGGAGGAGGA CCCGGGGAGG 60

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GAGGCGCGGC GCGGGAGGAG GAGGGGCGCA GCCGCGGAGC CAGTGGCCCC GCTTGGACGC 120
GCTGCTCTCC AGATAACCCC GGAGCTCCAG CCGCGCGGAT CGCGCGCTCC CGCCGCTCTG 180
CCCCTAAACT TCTGCCGTAG CTCCCTTTCA AGCCAGCGAA TTTATTCCTT AAAACCAGAA 240
ACTGAACCTC GGCACGGGAA AGGAGTCCGC GGAGGAGCAA AACCACAGCA GAGCAAGAAG 300
AGCTTCAGAG AGCAGCCTTC CCGGAGCACC AACTCCGTGT CGGGAGTGCA GAAACCAACA 360
AGTGAGAGGG CGCCGCGTTC CCGGGGCGCA GCTGCGGGCG GCGGGAGCAG GCGCAGGAGG 420
AGGAAGCGAG CGCCCCCGAG CCCCAGAGCCC GAGTCCCCGA GCCTGAGCCG CAATCGCTGC 480
GGTACTCTGC TCCGGATTTC TGTGCGCGGG CTCGCCGAGC GCTGGGCAGG AGGCTTCGTT 540
TTGCCCTGGT TGCAAGCAGC GGCTGGGAGC AGCCGGTCCC TGGGGAATAT GCGGCGCGCG 600
TGGATCCTGC TCACCTTGGG CTTGGTGGCC TCGTGTTCGG CGGAGTCGAG AGCAGAGCTG 660
ACATCTGATA AAGACATGTA CCTTGACAAC AGCTCCATTG AAGAAGCTTC AGGAGTGTAT 720
CCTATTGATG ACGATGACTA CGCTTCTGCG TCTGGCTCGG GAGCTGATGA GGATGTAGAG 780
AGTCCAGAGC TGACAACAAC TCGACCACTT CCAAAGATAC TGTGACTAG TGCTGCTCCA 840
AAAGTGGAAG CCACGACGCT GAATATACAG AACAAGATAC CTGCTCAGAC AAAGTCACCT 900
GAAGAACTG ATAAAGAGAA AGTTCACCTC TCTGACTCAG AAAGGAAAAT GGACCCAGCC 960
GAAGAGGATA CAAATGTGTA TACTGAGAAA CACTCAGACA GTCTGTTTAA ACGGACAGAA 1020

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Gly Arg Arg Glu Gly Ala Arg Gly Lys Glu Glu Glu Glu Lys Glu Glu
1      5      10      15
Asp Pro Gly Arg Glu Ala Arg Arg Gly Arg Arg Arg Gly Ala Ala Ala
20      25      30
Glu Pro Val Ala Pro Leu Gly Arg Ala Ala Leu Gln Ile Pro Pro Glu
35      40      45
Leu Gln Pro Arg Gly Ser Arg Ala Pro Ala Ala Leu Pro Leu Asn Phe
50      55      60
Cys Arg Ser Ser Leu Ser Ser Gln Arg Ile Tyr Ser Leu Lys Pro Glu
65      70      75      80
Thr Glu Pro Arg His Gly Lys Gly Val Arg Gly Gly Ala Lys Pro Gln
85      90      95
Gln Ser Lys Lys Ser Phe Arg Glu Gln Pro Ser Arg Ser Thr Asn Ser
100     105     110
Val Ser Gly Val Gln Lys Pro Thr Ser Glu Arg Ala Pro Arg Ser Arg
115     120     125
Gly Ala Ala Ala Gly Gly Gly Ser Arg Arg Arg Arg Arg Lys Arg Ala
130     135     140
Pro Pro Ser Pro Glu Pro Glu Ser Pro Ser Leu Ser Arg Asn Arg Cys
145     150     155     160
Gly Thr Leu Leu Arg Ile Arg Val Arg Gly Leu Ala Glu Arg Trp Ala
165     170     175
Gly Gly Phe Val Leu Pro Trp Leu Gln Ala Ala Ala Gly Ser Ser Arg
180     185     190
Ser Leu Gly Asn Met Arg Arg Ala Trp Ile Leu Leu Thr Leu Gly Leu
195     200     205
Val Ala Cys Val Ser Ala Glu Ser Arg Ala Glu Leu Thr Ser Asp Lys
210     215     220
Asp Met Tyr Leu Asp Asn Ser Ser Ile Glu Glu Ala Ser Gly Val Tyr
225     230     235     240
Pro Ile Asp Asp Asp Asp Tyr Ala Ser Ala Ser Gly Ser Gly Ala Asp
245     250     255
Glu Asp Val Glu Ser Pro Glu Leu Thr Thr Thr Arg Pro Leu Pro Lys
260     265     270
Ile Leu Leu Thr Ser Ala Ala Pro Lys Val Glu Thr Thr Thr Leu Asn
275     280     285

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Ile	Gln	Asn	Lys	Ile	Pro	Ala	Gln	Thr	Lys	Ser	Pro	Glu	Glu	Thr	Asp
290						295					300				
Lys	Glu	Lys	Val	His	Leu	Ser	Asp	Ser	Glu	Arg	Lys	Met	Asp	Pro	Ala
305					310					315					320
Glu	Glu	Asp	Thr	Asn	Val	Tyr	Thr	Glu	Lys	His	Ser	Asp	Ser	Leu	Phe
				325					330					335	
Lys	Arg	Thr	Glu												
			340												

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1079 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCCCCGCGC	GCTGCTGAGC	CGTCCTTGCG	GCACGSSGAT	GCCCCGCGGAG	CTGCGGCGGCC	60
TCGCGGTGCT	GCTGCTGCTG	CTCAGCGCCC	GCGCAGCGCT	GGCTCAGCCG	TGGCGCAATG	120
AGAACTACGA	GAGGCCGGTG	GACCTGGAGG	GCTCTGGGGA	TGATGATCCC	TTTGGGGACG	180
ATGAACTGGA	TGACATCTAC	TCGGGCTCCG	GCTCAGGCTA	TTTTGAGCAG	GAGTCAGGGT	240
TGGAGACAGC	GGTCAGCCTC	ACCACGGACA	CGTCCGTCCC	ACTGCCCACC	ACGGTGGCCG	300
TGCTGCCTGT	CACCTTGGTG	CAGCCCATGG	CAACACCCTT	TGAGCTGTTC	CCCACAGAGG	360
ACACGTCCCC	TGAGCAAACA	ACCAGCGTCT	TGTATATCCC	CAAGATAACA	GAAGCACCAG	420
TGATCCCCAG	CTGGAAAACA	ACCACCGCCA	GTACCACTGC	CAGTGACTCC	CCCAGTACCA	480
CCTCCACCAC	CACCACCACG	GCTGCTACCA	CCACCACAAC	CACCACCACC	ATCAGCACCA	540
CTGTGGCCAC	CTCCAAGCCC	ACCACTACCC	AGAGGTTTCT	GCCCCCTTTT	GTCACCAAGG	600
CAGCCACCAC	CCGGGCCACC	ACCCTGGAGA	CGCCCACCAC	CTCCATCCCT	GAAACCAGTG	660
TCCTGACAGA	GGTGACCACA	TCACGGCTTG	TCCCCTCCAG	CACAGCCAAG	CCGAGGTCCC	720
TGCCAAAACC	AAGCACTTCC	AGGACTGCAG	AACCCACGGA	AAAAAGCACT	GCCTTGCCTT	780
CCAGCCCCAC	CACGCTGCCA	CCCACAGAAG	CCCCCCAGGT	GGAGCCAGGG	GAGTTGACGA	840
CAGTCCTCGA	CAGTGACCTG	GAAGTCCCAA	CCAGTAGTGG	CCCCAGCGGG	GACTTCGAGA	900
TCCAGGAGGA	GGAGGAGACA	ACTCGTCCTG	AGCTGGGCAA	TGAGGTGGTG	GCAGTGGTGA	960
CACCACCAGC	AGCACCGGGG	CTGGGCAAGA	ATGCAGAGCC	GGGGCTCATC	GACAACACAA	1020
TAGAGTCGGG	CAGCTCGGCT	GCTCAGCTCC	CCCAGAAAAA	CATCCTGGAG	AGGAAGGAA	1079

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCGCCTG	TCTGCCTGTT	TGCGCCGCTG	CTGCTGTTGC	TCCTCGGAGG	TTTCCCCGTC	60
GCCCCAGGCG	AGTCGATTCG	AGAGACTGAG	GTCATAGACC	CCCAGGACCT	CCTGGAAGGC	120
AGATACTTCT	CTGGAGCCCT	CCCGGACGAT	GAAGACGCTG	GGGGCCTTGA	GCAGGACTCT	180
GACTTTGAGC	TGTCGGGTTC	CGGAGATCTA	GATGACACGG	AGGAGCCCAG	GACCTTCCCT	240
GAGGTGATTT	CACCCTTGGT	GCCACTAGAT	AACCACATCC	CCGAGAATGC	CCAGCCTGGC	300
ATCCGTGTCC	CCTCAGAGCC	CAAGGAACTG	GAAGAGAATG	AGGTCATTCC	CAAAAGGGTC	360
CCCTCCGACG	TGGGGGATGA	CGATGTGTCC	AACAAAGTGT	CCATGTCCAG	CACTTCCCAG	420
GGCAGCAACA	TTTTTGAAAG	AACTGAG				447

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

SEP 15 2003
 10:00 AM
 10:00 AM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCCTAGCAG CTGTCATTGC TGGTGGAGTT ATTGGCTTTC TCTTTGCAAT TTTTCTTATC 60
CTGCTGTTGG TG 72

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Leu Ala Ala Val Ile Ala Gly Gly Val Ile Gly Phe Leu Phe Ala
1 5 10 15
Ile Phe Leu Ile Leu Leu Val
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTGTTGATAG CTGTGATTGT CGGCGGTGTG GTGGGAGCCC TCTTTGCTGC CTTCTTGTC 60
ATGCTGCTCA TCTAC 75

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCTTGGCAG CTCTGATTGT GGGCGGCGTA GTGGGCATCC TCTTCGCCGT TTTCTTGATC 60
CTGCTGCTGG TGTAC 75

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCGCCACTC GCCCAGAGCC TCACTACTTC TTTCTGCTCT TCCTGTTCAC CTTGGTCCTT 60
GCTGCAGCCA GGCCCAGGTG GCGGTAAGTG CCC 93

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala Thr Arg Pro Glu Pro His Tyr Phe Phe Leu Leu Phe Leu Phe Thr
1 5 10 15

Leu Val Leu Ala Ala Ala Arg Pro Arg Trp Arg
20 25

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGCGACACT GCTCATCCCA GCCATCACGA CTGCTGACGC CGGCTTCTAC CTCTGCGTGG 60
CCACCAGCCC TGCAGGCACT GCC 83

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCATGAAGA AGAAGGATGA AGGCAGTTAC GACTTGGGCA AGAAACCCAT CTACAAAAAA 60
GCCCCACCA ACGAGTTCTA CGCATGA 87

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Gly Lys Lys Pro Ile Tyr Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCCGCCAGC AAGAGCCGGA GCT 23

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTGAGGCTCT GGGCGAGTGG GGG 23

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATAGAGCTCT TGGAACCATG GCGCCTGTCT GCC 33

(2) INFORMATION FOR SEQ ID NO:21:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGAATTCCAG GTTTTATTAT CTTTTTATC 29

(2) INFORMATION FOR SEQ ID NO:22:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGTATTGGGC GCCGTGTCAC CAGGGC 26

(2) INFORMATION FOR SEQ ID NO:23:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCCATGAGC TCCACCACCC TGTTTCG 26

(2) INFORMATION FOR SEQ ID NO:24:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Leu Gly Lys Lys Pro Ile Tyr Lys Lys 9
1 5

(2) INFORMATION FOR SEQ ID NO:25:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Glu Phe Tyr Ala 4
1

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